GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: August 27, 2001, 13:46:47 ; Search time 177.11 Seconds
(without alignments)
9781.382 Million cell updates/sec

Title: US-09-784-340-1
Perfect score: 2759
Sequence: 1 caaccattgcagatcagtgt.....ctgtcagccgttacgtagcg 2759

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 730101 seqs, 313950809 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_0601:*
1: /SIDS1/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn/NA1985.DAT:*
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9: /SIDS1/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:*
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20: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	551	20.0	1650	21	AAC65396	Human carbohydrate
2	484	17.5	515	20	AAV87412	EST clone BR77. H
3	350	12.7	350	21	AAC03286	Human secreted pro
4	35	1.3	978	21	AAZ95211	Human UGT2B15 exon
5	35	1.3	1976	21	AAZ95206	Human UDP-glucuron
6	32	1.2	2107	19	AAV15900	Uridine diphospho-
7	29	1.1	2092	21	AAZ95199	Human UDP-glucuron
8	28	1.0	480	21	AAZ95209	Human UGT2B15 exon
9	28	1.0	1362	19	AAV32421	Homo sapiens clone
10	27	1.0	930	22	AAF33114	Human secreted pro
11	27	1.0	1138	21	AAZ95196	Human UGT2B4 exon
12	27	1.0	1316	21	AAZ55915	Arabidopsis thalia
13	27	1.0	1380	22	AAF33111	Human secreted pro
14	27	1.0	1721	22	AAF63820	Human secreted pro
15	27	1.0	3426	22	AAC67268	Human NFAR-1 codin
16	27	1.0	3464	22	AAC91232	Human DHFR gene ex
17	26	0.9	1069	20	AAX06970	Mouse secretory pe
18	26	0.9	1069	21	AAZ08294	Mouse ortholog gen
19	26	0.9	1200	21	AAF15723	Human prostate can
20	26	0.9	1375	20	AAZ41371	Human normal uteru
21	26	0.9	1602	21	AAZ95210	Human UGT2B15 exon
22	25	0.9	48	20	AAZ11021	Probe PL-3 for HIV
c 23	25	0.9	61	21	AAC29871	Human secreted pro
c 24	25	0.9	72	20	AAZ11017	Probe OL-1 for HIV
c 25	25	0.9	75	20	AAZ11018	Probe OL-4 for HIV
c 26	25	0.9	175	21	AAC13071	Human secreted pro
27	25	0.9	282	20	AAV86663	EST clone BF314.
28	25	0.9	302	21	AAC98700	Human colon cancer
29	25	0.9	349	21	AAC94854	Cat flea hindgut a
c 30	25	0.9	396	22	AAF94934	Human ovarian canc
31	25	0.9	492	21	AAC93696	Cat flea hindgut a
32	25	0.9	524	21	AAA96571	Noncoding region o
33	25	0.9	557	21	AAA06603	Human immunogenic
c 34	25	0.9	569	21	AAZ80477	Human colon cancer
35	25	0.9	661	20	AAV84479	Human secreted pro
36	25	0.9	747	20	AAX30361	DNA encoding a hum
37	25	0.9	777	19	AAV59681	Human secreted pro
38	25	0.9	890	20	AAX37519	Human secreted pro
c 39	25	0.9	900	21	AAF08617	Fusarium venenatum
40	25	0.9	957	11	AAQ04441	Aequorin gene. Ae
41	25	0.9	958	22	AAC92233	Apoaequorin-encodi
42	25	0.9	959	9	AAN81534	pAQ440 aequorin ge
43	25	0.9	1093	21	AAC77825	Human cancer assoc
44	25	0.9	1179	21	AAC47833	Arabidopsis thalia
c 45	25	0.9	1187	21	AAC52841	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAC65396
ID AAC65396 standard; cDNA; 1650 BP.
XX
AC AAC65396;
XX
DT 13-FEB-2001 (first entry)
XX
DE Human carbohydrate-modifying enzyme cDNA Incyte ID No: 2912330CB1.
XX
KW Human; carbohydrate-modifying enzyme; CME; antidiabetic;
KW immunosuppressive; anti-HIV; antiinflammatory; antianaemic;
KW antiasthmatic; antiarteriosclerotic; antithyroid; hepatotropic;
KW nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic;
KW antiarthritic; antipsoriatic; uropathic; ophthalmological;
KW dermatological; antiulcer; cytostatic; viruicide; antibacterial;
KW fungicide; protozoacide; tranquiliser; vulnerary; diabetes;
KW autoimmune disorder; inflammatory disorder; infection; ss.
XX
OS Homo sapiens.
XX
PN WO200063351-A2.
XX
PD 26-OCT-2000.
XX
PF 20-APR-2000; 2000WO-US10882.
XX
PR 21-APR-1999; 99US-0130383.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Yue H, Tang YT, Hillman JL, Baughn MR, Yang J;
XX
DR WPI; 2000-672729/65.

```
DR   P-PSDB; AAB28677.
XX
PT   Novel carbohydrate modifying enzyme polypeptides and polynucleotides
PT   for diagnosis, treatment, and prevention of carbohydrate metabolism
PT   disorders, autoimmune/inflammatory disorders, and cancer -
XX
PS   Claim 4; Page 75; 75pp; English.
XX
CC   The present cDNA sequence encodes a human carbohydrate-modifying enzyme
CC   (CME). CME polynucleotides and polypeptides are useful for treating and
CC   diagnosing diseases associated with CME such as diabetes,
CC   autoimmune/inflammatory disorders such as AIDS, Addison's disease,
CC   adult respiratory distress syndrome, allergies, anaemia, asthma,
CC   atherosclerosis, autoimmune thyroiditis, bronchitis, cholocystitis,
CC   contact dermatitis, Crohn's disease, emphysema, erythroblastosis fetalis,
CC   glomerulonephritis, Good pasture's syndrome, gout, Grave's disease,
CC   Hashimoto's thyroiditis, multiple sclerosis, myasthenia gravis,
CC   osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,
CC   Reiter's syndrome, arthritis, scleroderma, sjogren's syndrome, systemic
CC   lupus erythematosus, ulcerative colitis, uveitis, Werner syndrome,
CC   complications of cancer, haemodialysis, and extracorporeal circulation,
CC   viral, bacterial, fungal parasitic, protozoal, and helminthic infections,
CC   trauma, or cancer. CME, or its catalytic or immunogenic fragment, is
CC   useful for drug screening.
XX
SQ   Sequence 1650 BP; 489 A; 330 C; 354 G; 477 T; 0 other;

  Query Match             20.0%;  Score 551;  DB 21;  Length 1650;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-189;
  Matches  551;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1097 tggataccccagaatgatcttcttggtcatcccaaaaccaaagcttttatcactcatggt 1156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1100 tggataccccagaatgatcttcttggtcatcccaaaaccaaagcttttatcactcatggt 1159

Qy   1157 ggaatgaatgggatctatgaagctatttaccatggggtccctatggtgggagttcccata 1216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1160 ggaatgaatgggatctatgaagctatttaccatggggtccctatggtgggagttcccata 1219

Qy   1217 tttggtgatcagcttgataacatagctcacatgaaggccaaaggagcagctgtagaaata 1276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1220 tttggtgatcagcttgataacatagctcacatgaaggccaaaggagcagctgtagaaata 1279

Qy   1277 aacttcaaaactatgacaagcgaagatttactgagggctttgagaacagtcattaccgat 1336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1280 aacttcaaaactatgacaagcgaagatttactgagggctttgagaacagtcattaccgat 1339

Qy   1337 tcctcttataaagagaatgctatgagattatcaagaattcaccatgatcaacctgtaaag 1396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1340 tcctcttataaagagaatgctatgagattatcaagaattcaccatgatcaacctgtaaag 1399

Qy   1397 cccctagatcgagcagtcttctggatcgagtttgtcatgcgccacaaaggagccaagcac 1456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1400 cccctagatcgagcagtcttctggatcgagtttgtcatgcgccacaaaggagccaagcac 1459

Qy   1457 ctgcgatcagctgcccatgacctcacctggttccagcactactctatagatgtgattggg 1516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1460 ctgcgatcagctgcccatgacctcacctggttccagcactactctatagatgtgattggg 1519

Qy   1517 ttcctgctgacctgtgtggcaactgctatattcttgttcacaaaatgtttttttatttttcc 1576
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1520 ttcctgctgacctgtgtggcaactgctatattcttgttcacaaaatgtttttttatttttcc 1579

Qy   1577 tgtcaaaaatttaataaaactagaaagatagaaaagagggaatagatctttccaaattca 1636
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1580 tgtcaaaaatttaataaaactagaaagatagaaaagagggaatagatctttccaaattca 1639

Qy   1637 agaaagacctg 1647
          ||||||||||||
Db   1640 agaaagacctg 1650
```

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RESULT   2
AAV87412
ID   AAV87412 standard; cDNA; 515 BP.
XX
AC   AAV87412;
XX
DT   27-APR-1999  (first entry)
XX
DE   EST clone BR77.
XX
KW   Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW   tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW   chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW   receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
OS   Homo sapiens.
XX
PN   WO9845435-A2.
XX
PD   15-OCT-1998.
XX
PF   10-APR-1998;   98WO-US06954.
XX
PR   10-APR-1997;   97US-0835913.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Agostino MJ,  Jacobs K,  Lavallie ER,  McCoy JM,  Merberg D;
PI   Racie LA,  Spaulding V,  Treacy M;
XX
DR   WPI; 1999-070076/06.
XX
PT   New polynucleotides encoding human secreted proteins - derived from
PT   e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT   ovary, pituitary, retina and colon cDNA libraries
XX
PS   Claim 1; Page 556; 633pp; English.
XX
CC   This sequence represents an expressed sequence tag (EST), and is a
CC   polynucleotide of the invention. The polynucleotides of the invention are
CC   all secreted EST sequences isolated from a variety of human tissue
CC   sources. The EST sequences and proteins encoded by them are predicted to
CC   have useful biological activities which would make them suitable for
CC   treating, preventing or ameliorating medical conditions in humans and
CC   animals, although no supporting data is given. Suggested activities
CC   include nutritional activity, immune stimulating or suppressing activity,
CC   haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC   activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC   activity. The EST sequences are also stated to be useful for gene
CC   therapy.
XX
SQ   Sequence 515 BP; 148 A; 98 C; 122 G; 147 T; 0 other;

  Query Match             17.5%;  Score 484;  DB 20;  Length 515;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-165;
  Matches  484;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     27 gaactgccatcatgaggtctgacaagtcagctttggtatttctgctcctgcagctcttct 86
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22 gaactgccatcatgaggtctgacaagtcagctttggtatttctgctcctgcagctcttct 81

Qy     87 gtgttggctgtggattctgtgggaaagtcctggtgtggccctgtgacatgagccattggc 146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 gtgttggctgtggattctgtgggaaagtcctggtgtggccctgtgacatgagccattggc 141

Qy    147 ttaatgtcaaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattga 206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 ttaatgtcaaggtcattctagaagagctcatagtgagaggccatgaggtaacagtattga 201

Qy    207 ctcactcaaagccttcgttaattgactacaggaagccttctgcattgaaatttgaggtgg 266
```

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 ctcactcaaagccttcgttaattgactacaggaagccttctgcattgaaatttgaggtgg 261

Qy    267 tccatatgccacaggacagaacagaagaaaatgaaatatttgttgacctagctctgaatg 326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    262 tccatatgccacaggacagaacagaagaaaatgaaatatttgttgacctagctctgaatg 321

Qy    327 tcttgccaggcttatcaacctggcaatcagttataaaattaaatgatttttttgttgaaa 386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 tcttgccaggcttatcaacctggcaatcagttataaaattaaatgatttttttgttgaaa 381

Qy    387 taagaggaactttaaaaatgatgtgtgagagctttatctacaatcagacgcttatgaaga 446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 taagaggaactttaaaaatgatgtgtgagagctttatctacaatcagacgcttatgaaga 441

Qy    447 agctacaggaaaccaactacgatgtaatgcttatagaccctgtgattccctgtggagacc 506
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 agctacaggaaaccaactacgatgtaatgcttatagaccctgtgattccctgtggagacc 501

Qy    507 tgat 510
          ||||
Db    502 tgat 505


RESULT   3
AAC03286
ID   AAC03286 standard; cDNA; 350 BP.
XX
AC   AAC03286;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 3284.
XX
KW   Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW   gene therapy; chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
PR   26-FEB-1999;   99US-0122487.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Duclert A,  Giordano J;
XX
DR   WPI; 2000-500381/45.
DR   P-PSDB; AAG03280.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS   Claim 1; SEQ ID 3284; 71pp + CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. An ORF has been identified within the
CC   sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC   derived from 30 different tissues. EST sequences usually correspond
CC   mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC   often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC   well suited for isolating cDNA sequences derived from the 5' ends of
CC   mRNAs and even in those cases where longer cDNA sequences have been
CC   obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC   mRNAs with intact 5' ends and can therefore be used to obtain full length
CC   cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC   gene therapy and chromosome mapping procedures. They are used to obtain
CC   upstream regulatory sequences and to design expression and secretion
CC   vectors.
XX
SQ   Sequence 350 BP; 108 A; 69 C; 77 G; 96 T; 0 other;


  Query Match             12.7%;  Score 350;  DB 21;  Length 350;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-117;
  Matches  350;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    791 gagatatggctaatacgaacatattgggattttgaatttcctcaaccataccaacctaac 850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 gagatatggctaatacgaacatattgggattttgaatttcctcaaccataccaacctaac 60

Qy    851 tttgagtttgttggaggattgcactgtaaacctgccaaagttttgcctaaggaaatggaa 910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 tttgagtttgttggaggattgcactgtaaacctgccaaagttttgcctaaggaaatggaa 120

Qy    911 aattttgtccagagttcaggggaagatggtattgtggtgttttctctggggtcactgttt 970
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 aattttgtccagagttcaggggaagatggtattgtggtgttttctctggggtcactgttt 180

Qy    971 caaaatgttacagaagaaaaggctaatatcattgcttcagcccttgcccagatcccacag 1030
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 caaaatgttacagaagaaaaggctaatatcattgcttcagcccttgcccagatcccacag 240

Qy   1031 aaggtgttatggaggtacaaaggaaaaaaaaccatccacattaggagccaatactcggctg 1090
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 aaggtgttatggaggtacaaaggaaaaaaaaccatccacattaggagccaatactcggctg 300

Qy   1091 tatgattggataccccagaatgatcttcttggtcatcccaaaaccaaagc 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 tatgattggataccccagaatgatcttcttggtcatcccaaaaccaaagc 350


RESULT   4
AAZ95211
ID   AAZ95211 standard; DNA; 978 BP.
XX
AC   AAZ95211;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UGT2B15 exon 5 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B15; UGT2B15; polymorphism; metabolism;
KW   drug interaction; detect; human; single nucleotide polymorphism;
KW   SNPs; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions -
XX
PS   Example 3; Page 62; 72pp; English.
XX
CC   This sequence represents the nucleotide sequence of exon 5 of the human
CC   UDP-glucuronosyltransferase 2B15 (UGT2B15) gene.
CC   UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
```

CC the glucuronic acid conjugation of a wide range of endogenous and
CC exogenous substrates. The UGT2B gene subfamily encode steroid
CC metabolizing isoforms in the liver. Alteration of the expression or
CC function of UGTs may effect drug metabolism. The invention relates to
CC non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC can be used to detect altered UGT2B metabolism of a substrate in an
CC individual. The nucleic acid molecules comprising a human UGT2B sequence
CC polymorphism can be used in screening assays for genotyping individuals,
CC also to predict their rate of metabolism of UGT2B substrate, potential
CC drug-drug interactions and adverse side effects. The polymorphisms can be
CC used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC linkage related to phenotypic variation in activity or expression of
CC UGT2B protein. The polymorphism containing nucleic acid molecules may
CC also be used for generating genetically modified non-human animals and
CC for obtaining site specific gene modification in cell lines.
XX
SQ Sequence 978 BP; 321 A; 187 C; 162 G; 308 T; 0 other;

Query Match 1.3%; Score 35; DB 21; Length 978;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1424 gagtttgtcatgcgccacaaaggagccaagcacct 1458
||||||||||||||||||||||||||||||||||||
Db 408 gagtttgtcatgcgccacaaaggagccaagcacct 442

RESULT 5
AAZ95206
ID AAZ95206 standard; DNA; 1976 BP.
XX
AC AAZ95206;
XX
DT 05-JUN-2000 (first entry)
XX
DE Human UDP-glucuronosyltransferase 2B15 nucleotide sequence.
XX
KW UDP-glucuronosyltransferase 2B15; UGT2B15; polymorphism; metabolism;
KW drug interaction; detect; human; single nucleotide polymorphism;
KW SNPs; ds.
XX
OS Homo sapiens.
XX
PN WO200006776-A1.
XX
PD 10-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16675.
XX
PR 28-JUL-1998; 98US-0094391.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, Penny L, Riedy M;
XX
DR WPI; 2000-195321/17.
DR P-PSDB; AAY78935.
XX
PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT genotyping individuals to predict rate of metabolism of substrates and
PT for identifying potential drug interactions -
XX
PS Disclosure; Page 56-59; 72pp; English.
XX
CC This sequence represents the human UDP-glucuronosyltransferase 2B15
CC (UGT2B15) gene. UDP-glucuronosyltransferase (UGTs) are a family of
CC enzymes that catalyse the glucuronic acid conjugation of a wide range of
CC endogenous and exogenous substrates. The UGT2B gene subfamily encode
CC steroid metabolizing isoforms in the liver. Alteration of the expression
CC or function of UGTs may effect drug metabolism. The invention relates to
CC non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC sequence polymorphisms (see AAZ95051-Z95110). Probes which detect the
CC UGT2B locus polymorphisms can be used to detect altered UGT2B metabolism
CC of a substrate in an individual. The nucleic acid molecules comprising a
CC human UGT2B sequence polymorphism can be used in screening assays for
CC genotyping individuals, also to predict their rate of metabolism of
CC UGT2B substrate, potential drug-drug interactions and adverse side
CC effects. The polymorphisms can be used as single nucleotide polymorphisms
CC (SNPs) for detecting genetic linkage related to phenotypic variation in
CC activity or expression of UGT2B protein. The polymorphism containing
CC nucleic acid molecules may also be used for generating genetically
CC modified non-human animals and for obtaining site specific gene
CC modification in cell lines.
XX
SQ Sequence 1976 BP; 594 A; 368 C; 419 G; 595 T; 0 other;

Query Match 1.3%; Score 35; DB 21; Length 1976;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1424 gagtttgtcatgcgccacaaaggagccaagcacct 1458
||||||||||||||||||||||||||||||||||||
Db 1406 gagtttgtcatgcgccacaaaggagccaagcacct 1440

RESULT 6
AAV15900
ID AAV15900 standard; cDNA; 2107 BP.
XX
AC AAV15900;
XX
DT 26-MAY-1998 (first entry)
XX
DE Uridine diphospho-glucuronosyltransferase 2B17 (UGT2B17) encoding cDNA.
XX
KW Uridine diphospho-glucuronosyltransferase 2B17; UGT2B17; catalyse;
KW androsterone; androsterone-glucuronic acid; androgen; enzyme; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..51
FT /*tag= a
FT CDS 52..1644
FT /*tag= b
FT /product= "UGTB17 enzyme"
FT 3'UTR 1645..2107
FT /*tag= c
XX
PN WO9744466-A1.
XX
PD 27-NOV-1997.
XX
PF 16-MAY-1997; 97WO-CA00328.
XX
PR 17-MAY-1996; 96US-0649319.
XX
PA (ENDO-) ENDORECHERCHE INC.
XX
PI Beaulieu M, Belanger A, Hum DW, Levesque E;
XX
DR WPI; 1998-018520/02.
DR P-PSDB; AAW47126.
XX
PT DNA encoding uridine di:phospho:glucuronosyl:transferase 2B17 -
PT which catalyses conversion of androsterone to
PT androsterone-glucuronic acid
XX
PS Claim 15; Pages 4-6; 53pp; English.
XX
CC This cDNA encodes an enzyme uridine di-phosphoglucuronosyltransferase
CC 2B17 (UGT2B17). This novel enzyme catalyses the conversion of
CC androsterone to androsterone-glucuronic acid. The UGT2B17 can be used to

```
CC   detect anti-UGT2B17 antibodies. The antibody can be used to detect a
CC   localised concentration of UGT2B17 or an alteration in androgen activity.
CC   The UGT2B17 can also be used to alter the concentration of an androgenic
CC   compound in a tissue, specifically dihydrotestosterone. An isolated
CC   nucleotide sequence comprising at least 30 consecutive nucleotides from
CC   the coding region of the 2107 base pair sequence, or its complement can
CC   be used to block the synthesis of UGT2B17, e.g. an expression disrupting
CC   sense or antisense fragment, or as a probe for a UGT2B17 coding sequence.
XX
SQ   Sequence 2107 BP; 657 A; 382 C; 424 G; 644 T; 0 other;


  Query Match             1.2%;  Score 32;  DB 19;  Length 2107;
  Best Local Similarity   100.0%;  Pred. No. 0.0084;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1115 cttcttggtcatcccaaaaccaaagcttttat 1146
           ||||||||||||||||||||||||||||||||
Db   1138 cttcttggtcatcccaaaaccaaagcttttat 1169


RESULT   7
AAZ95199
ID   AAZ95199 standard; DNA; 2092 BP.
XX
AC   AAZ95199;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UDP-glucuronosyltransferase 2B4 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B4; UGT2B4; polymorphism; metabolism; SNPs;
KW   drug interaction; detect; human; single nucleotide polymorphism; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
DR   P-PSDB; AAY78933.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions -
XX
PS   Disclosure; Page 34-36; 72pp; English.
XX
CC   This sequence represents the human UDP-glucuronosyltransferase 2B4
CC   (UGT2B4) gene. UDP-glucuronosyltransferase (UGTs) are a family of
CC   enzymes that catalyse the glucuronic acid conjugation of a wide range of
CC   endogenous and exogenous substrates. The UGT2B gene subfamily encode
CC   steroid metabolizing isoforms in the liver. Alteration of the expression
CC   or function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms (see AAZ95051-Z95110). Probes which detect the
CC   UGT2B locus polymorphisms can be used to detect altered UGT2B metabolism
CC   of a substrate in an individual. The nucleic acid molecules comprising a
CC   human UGT2B sequence polymorphism can be used in screening assays for
CC   genotyping individuals, also to predict their rate of metabolism of
CC   UGT2B substrate, potential drug-drug interactions and adverse side
CC   effects. The polymorphisms can be used as single nucleotide polymorphisms
CC   (SNPs) for detecting genetic linkage related to phenotypic variation in
CC   activity or expression of UGT2B protein. The polymorphism containing
CC   nucleic acid molecules may also be used for generating genetically
CC   modified non-human animals and for obtaining site specific gene
CC   modification in cell lines.
XX
SQ   Sequence 2092 BP; 639 A; 398 C; 438 G; 617 T; 0 other;


  Query Match             1.1%;  Score 29;  DB 21;  Length 2092;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1097 tggataccccagaatgatcttcttggtca 1125
           |||||||||||||||||||||||||||||
Db   1103 tggataccccagaatgatcttcttggtca 1131


RESULT   8
AAZ95209
ID   AAZ95209 standard; DNA; 480 BP.
XX
AC   AAZ95209;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human UGT2B15 exon 3 nucleotide sequence.
XX
KW   UDP-glucuronosyltransferase 2B15; UGT2B15; polymorphism; metabolism;
KW   drug interaction; detect; human; single nucleotide polymorphism;
KW   SNPs; ds.
XX
OS   Homo sapiens.
XX
PN   WO200006776-A1.
XX
PD   10-FEB-2000.
XX
PF   22-JUL-1999;   99WO-US16675.
XX
PR   28-JUL-1998;   98US-0094391.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Galvin M,  Miller A,  Penny L,  Riedy M;
XX
DR   WPI; 2000-195321/17.
XX
PT   Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT   genotyping individuals to predict rate of metabolism of substrates and
PT   for identifying potential drug interactions -
XX
PS   Example 3; Page 61; 72pp; English.
XX
CC   This sequence represents the nucleotide sequence of exon 3 of the human
CC   UDP-glucuronosyltransferase 2B15 (UGT2B15) gene.
CC   UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC   the glucuronic acid conjugation of a wide range of endogenous and
CC   exogenous substrates. The UGT2B gene subfamily encode steroid
CC   metabolizing isoforms in the liver. Alteration of the expression or
CC   function of UGTs may effect drug metabolism. The invention relates to
CC   non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC   sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC   can be used to detect altered UGT2B metabolism of a substrate in an
CC   individual. The nucleic acid molecules comprising a human UGT2B sequence
CC   polymorphism can be used in screening assays for genotyping individuals,
CC   also to predict their rate of metabolism of UGT2B substrate, potential
CC   drug-drug interactions and adverse side effects. The polymorphisms can be
CC   used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC   linkage related to phenotypic variation in activity or expression of
CC   UGT2B protein. The polymorphism containing nucleic acid molecules may
CC   also be used for generating genetically modified non-human animals and
CC   for obtaining site specific gene modification in cell lines.
XX
SQ   Sequence 480 BP; 154 A; 75 C; 101 G; 150 T; 0 other;
```

```
  Query Match             1.0%;  Score 28;  DB 21;  Length 480;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     936 atggtattgtggtgttttctctggggtc 963
           ||||||||||||||||||||||||||||
Db      77 atggtattgtggtgttttctctggggtc 104


RESULT   9
AAV32421
ID   AAV32421 standard; cDNA; 1362 BP.
XX
AC   AAV32421;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Homo sapiens clone CC182_1 coding region.
XX
KW   Secreted protein; clone; CC182_1; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             405..662
FT                   /*tag=  a
FT                   /product= CC182_1 protein
XX
PN   WO9822501-A2.
XX
PD   28-MAY-1998.
XX
PF   19-NOV-1997;   97WO-US21123.
XX
PR   17-NOV-1997;   97US-0971786.
PR   20-NOV-1996;   96US-0752912.
PR   14-FEB-1997;   97US-0800826.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Agostino MJ,  Jacobs K,  Lavallie ER,  Mccoy JM,  Merberg D;
PI   Racie LA,  Spaulding V,  Treacy M;
XX
DR   WPI; 1998-312414/27.
DR   P-PSDB; AAW48807.
XX
PT   New nucleic acid encoding secreted protein from human cells -
PT   potentially useful, e.g. as immuno-modulators, antitumour agents,
PT   promoters of tissue growth, haemostatic and thrombolytic agents
XX
PS   Claim 28; Page 70; 93pp; English.
XX
CC   The sequence is that of the coding region of clone CC182_1. It
CC   encodes a secreted protein and may be used to express the protein
CC   recombinantly, as a tissue/molecular weight markers; for chromosome
CC   identification, to identify possible genetic disorders, to isolate
CC   new related DNA, as a source of primers for PCR, to generate
CC   anti-protein or anti-DNA antibodies and in interaction trap
CC   assays to identify sequences that encode interacting proteins. The
CC   protein can be used to screen compounds for biological activity, to
CC   raise antibodies, as tissue markers, for isolation of related receptors
CC   and ligands and as nutritional sources. Such proteins may also
CC   have many biological activities, e.g. cytokine and cell
CC   proliferation/differentiation activity; immunosuppressant or
CC   immunostimulant activity (e.g. for treating immune deficiency, including
CC   infection with human immune deficiency virus, regulation of lymphocyte
CC   growth, treating cancer and many autoimmune diseases, to prevent
CC   transplant rejection or induce tumour immunity), regulation of
CC   haematopoiesis, e.g. treatment of myeloid or lymphoid diseases;
CC   promoting growth of bone, cartilage, tendon, ligament and nerve tissue,
CC   e.g. for healing wounds, treatment of burns, ulcers, periodontal disease
CC   and neurodegeneration, inhibition or activation of follicle-stimulating
CC   hormone (modulation of fertility), chemotactic/chemokinetic activity
CC   (e.g. for mobilising specific cell types to sites of injury, infection),
CC   haemostatic and thrombolytic activity (e.g. for treating haemophilia or
CC   stroke), as receptors or ligands; antiflammatory activity (for treating
CC   septic shock, Crohn's disease etc.), as antimicrobials, modulators of
CC   metabolism and behaviour, as analgesics, enzymes for treating specific
CC   deficiency disorders and in treatment of psoriasis, in human or
CC   veterinary medicine. Neutralising antibodies against the protein can
CC   be used therapeutically, e.g. to detect or prevent metastasis of
CC   cancers expressing the protein. The protein can be expressed in
CC   vivo from DNA, introduced in standard gene therapy vectors.
XX
SQ   Sequence 1362 BP; 409 A; 210 C; 197 G; 544 T; 2 other;


  Query Match             1.0%;  Score 28;  DB 19;  Length 1362;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2527 ctgaaagtaaaaaaaaaaaaaaaaaaaa 2554
           ||||||||||||||||||||||||||||
Db    1322 ctgaaagtaaaaaaaaaaaaaaaaaaaa 1349


RESULT  10
AAF33114
ID   AAF33114 standard; cDNA; 930 BP.
XX
AC   AAF33114;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Human secreted protein gene 20 SEQ ID NO:30.
XX
KW   Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW   antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW   nootropic; neuroprotective; antibacterial; virucide; fungicide;
KW   opthalmalogical; autoimmune disease; hyperproliferative disorder;
KW   cardiovascular disorder; cerebrovascular disorder; infection; chemotaxis;
KW   nervous system disorder; ocular disorder; skin aging; wound healing;
KW   food additive; tissue regeneration; ss.
XX
OS   Homo sapiens.
XX
PN   WO200077256-A1.
XX
PD   21-DEC-2000.
XX
PF   01-JUN-2000; 2000WO-US14963.
XX
PR   11-JUN-1999;   99US-0138631.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM,  Komatsoulis GA;
XX
DR   WPI; 2001-032315/04.
DR   P-PSDB; AAB64792.
XX
PT   Isolated nucleic acid molecule encoding a human secreted protein is
PT   used in preventing, treating or ameliorating a medical condition -
XX
PS   Claim 1; Page 439; 506pp; English.
XX
CC   Polynucleotide sequences AAF33095 - AAF33142 encode human secreted
CC   proteins AAB64773 - AAB64820. Fragments of the secreted proteins and
CC   amino acid sequences which share homology with the fragments are
CC   represented in AAB64821 - AAB64880. The genes and proteins have
CC   activities dependent on the tissues and cells in which they are
CC   expressed. Examples of their activities and the activities of their
CC   agonists and antagonists include, immunosuppressive; antiarthritic;
CC   antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
```

CC cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
CC fungicide; and opthalmalogical. The secreted proteins, polynucleotides,
CC antagonists and agonists may be useful in treating, preventing and
CC diagnosing diseases and disorders such as autoimmune diseases e.g.
CC rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the
CC breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous
CC system disorders e.g. Alzheimer's disease, infections caused by bacteria,
CC viruses and fungi and ocular disorders e.g. corneal infection. The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. The polypeptides can also be
CC used as a food additive or preservative to increase or decrease storage
CC capabilities. Included in the invention are sequences AAB64772 and
CC AAF33095 - AAF33142 which are used in the isolation and characterisation
CC of the nucleotide and protein sequences of the invention.
XX
SQ Sequence 930 BP; 280 A; 137 C; 136 G; 376 T; 1 other;

Query Match 1.0%; Score 27; DB 22; Length 930;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2528 tgaaagtaaaaaaaaaaaaaaaaaaaa 2554
||||||||||||||||||||||||||||
Db 901 tgaaagtaaaaaaaaaaaaaaaaaaaa 927

RESULT 11
AAZ95196
ID AAZ95196 standard; DNA; 1138 BP.
XX
AC AAZ95196;
XX
DT 05-JUN-2000 (first entry)
XX
DE Human UGT2B4 exon 4 nucleotide sequence.
XX
KW UDP-glucuronosyltransferase 2B4; UGT2B4; polymorphism; metabolism; SNPs;
KW drug interaction; detect; human; single nucleotide polymorphism; ds.
XX
OS Homo sapiens.
XX
PN WO200006776-A1.
XX
PD 10-FEB-2000.
XX
PF 22-JUL-1999; 99WO-US16675.
XX
PR 28-JUL-1998; 98US-0094391.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Galvin M, Miller A, Penny L, Riedy M;
XX
DR WPI; 2000-195321/17.
XX
PT Novel human UDP-glucuronosyltransferase sequence, polymorphisms for
PT genotyping individuals to predict rate of metabolism of substrates and
PT for identifying potential drug interactions -
XX
PS Example 1; Page 32-33; 72pp; English.
XX
CC This sequence represents the nucleotide sequence of exon 4 of the human
CC UDP-glucuronosyltransferase 2B4 (UGT2B4) gene.
CC UDP-glucuronosyltransferase (UGTs) are a family of enzymes that catalyse
CC the glucuronic acid conjugation of a wide range of endogenous and
CC exogenous substrates. The UGT2B gene subfamily encode steroid
CC metabolizing isoforms in the liver. Alteration of the expression or
CC function of UGTs may effect drug metabolism. The invention relates to
CC non-chromosomal nucleic acid molecules, which comprise human UGT2B
CC sequence polymorphisms. Probes which detect the UGT2B locus polymorphisms
CC can be used to detect altered UGT2B metabolism of a substrate in an
CC individual. The nucleic acid molecules comprising a human UGT2B sequence
CC polymorphism can be used in screening assays for genotyping individuals,
CC also to predict their rate of metabolism of UGT2B substrate, potential
CC drug-drug interactions and adverse side effects. The polymorphisms can be
CC used as single nucleotide polymorphisms (SNPs) for detecting genetic
CC linkage related to phenotypic variation in activity or expression of
CC UGT2B protein. The polymorphism containing nucleic acid molecules may
CC also be used for generating genetically modified non-human animals and
CC for obtaining site specific gene modification in cell lines.
XX
SQ Sequence 1138 BP; 324 A; 220 C; 189 G; 405 T; 0 other;

Query Match 1.0%; Score 27; DB 21; Length 1138;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1097 tggataccccagaatgatcttcttggt 1123
||||||||||||||||||||||||||||
Db 458 tggataccccagaatgatcttcttggt 484

RESULT 12
AAZ55915
ID AAZ55915 standard; cDNA; 1316 BP.
XX
AC AAZ55915;
XX
DT 10-APR-2000 (first entry)
XX
DE Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox1 cDNA.
XX
KW Gibberellin 2-oxidase; AtGA2ox1; 2-beta-hydroxylation; inactivation;
KW growth inhibition; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 41..1030
FT /*tag= a
FT /product= "Gibberellin 2-oxidase AtGA2ox1"
XX
PN WO9966029-A2.
XX
PD 23-DEC-1999.
XX
PF 11-JUN-1999; 99WO-GB01857.
XX
PR 12-JUN-1998; 98GB-0012821.
PR 15-JUL-1998; 98GB-0015404.
XX
PA (UYBR-) UNIV BRISTOL.
XX
PI Thomas SG, Hedden P, Phillips AL;
XX
DR WPI; 2000-097742/08.
DR P-PSDB; AAY58598.
XX
PT New isolated plant gibberellin 2-oxidase enzymes and nucleic acids,
PT used to produce transgenic plants with improved or altered growth
PT characteristics -
XX
PS Example 3; Fig 5; 42pp; English.
XX
CC This sequence represents cDNA encoding an Arabidopsis thaliana
CC gibberellin (GA) 2-oxidase, PcGA2ox1. This enzyme is a GA 2-beta-
CC hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is
CC its only activity. Hydroxylation at the 2-beta position of a GA results
CC in a biologically inactive product, and is the most important route for
CC GA metabolism in plants, ensuring that the active hormones do not
CC accumulate in plant tissues. The nucleic acids can be used to transform

CC plants so that gibberellin 2-oxidase can be constitutively over-expressed
CC or otherwise enhanced to reduce the concentration of bioactive GAs in the
CC plants and therefore to inhibit plant growth. Growth inhibition is useful
CC in many agricultural and horticultural applications such as enhancing
CC lodging-resistance and grain yield in cereals, improving seedling
CC quality, reducing the growth of amenity grasses, reducing shoot growth in
CC orchard and ornamental trees, improving tolerance to cold, drought and
CC infection, and increasing yields (by the diversion of assimilates from
CC vegetative to reproductive organs). The nucleic acids may also be used to
CC induce male and/or female sterility (by expression in floral organs),
CC prevent pre-harvest sprouting, reduce shoot growth in hedging plants,
CC inhibit reversibility in the development or germination of seeds and
CC reduce shoot growth in commercial wood species. Antisense constructs of
CC the nucleic acids can also be used to transform plants to reduce the
CC expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to
CC improve fruit set and growth in seedless grapes, citrus fruits and
CC pears), improve skin texture and fruit shape in apples, increase stem
CC length and therefore yield in sugar cane, increase yield and earliness in
CC celery and rhubarb, improve malting yields and quality in cereals
CC (particularly barley), and increase growth in woody species.
XX
SQ Sequence 1316 BP; 440 A; 249 C; 252 G; 375 T; 0 other;

Query Match 1.0%; Score 27; DB 21; Length 1316;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2534 taaaaaaaaaaaaaaaaaaaacactgt 2560
||||||||||||||||||||||||||
Db 1190 taaaaaaaaaaaaaaaaaaaacactgt 1216

RESULT 13
AAF33111
ID AAF33111 standard; cDNA; 1380 BP.
XX
AC AAF33111;
XX
DT 23-MAR-2001 (first entry)
XX
DE Human secreted protein gene 17 SEQ ID NO:27.
XX
KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW nootropic; neuroprotective; antibacterial; virucide; fungicide;
KW opthalmalogical; autoimmune disease; hyperproliferative disorder;
KW cardiovascular disorder; cerebrovascular disorder; infection; chemotaxis;
KW nervous system disorder; ocular disorder; skin aging; wound healing;
KW food additive; tissue regeneration; ss.
XX
OS Homo sapiens.
XX
PN WO200077256-A1.
XX
PD 21-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US14963.
XX
PR 11-JUN-1999; 99US-0138631.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis GA;
XX
DR WPI; 2001-032315/04.
DR P-PSDB; AAB64789.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
PS Claim 1; Page 437-438; 506pp; English.
XX
CC Polynucleotide sequences AAF33095 - AAF33142 encode human secreted
CC proteins AAB64773 - AAB64820. Fragments of the secreted proteins and
CC amino acid sequences which share homology with the fragments are
CC represented in AAB64821 - AAB64880. The genes and proteins have
CC activities dependent on the tissues and cells in which they are
CC expressed. Examples of their activities and the activities of their
CC agonists and antagonists include, immunosuppressive; antiarthritic;
CC antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
CC cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
CC fungicide; and opthalmalogical. The secreted proteins, polynucleotides,
CC antagonists and agonists may be useful in treating, preventing and
CC diagnosing diseases and disorders such as autoimmune diseases e.g.
CC rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the
CC breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous
CC system disorders e.g. Alzheimer's disease, infections caused by bacteria,
CC viruses and fungi and ocular disorders e.g. corneal infection. The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. The polypeptides can also be
CC used as a food additive or preservative to increase or decrease storage
CC capabilities. Included in the invention are sequences AAB64772 and
CC AAF33095 - AAF33142 which are used in the isolation and characterisation
CC of the nucleotide and protein sequences of the invention.
XX
SQ Sequence 1380 BP; 351 A; 301 C; 270 G; 458 T; 0 other;

Query Match 1.0%; Score 27; DB 22; Length 1380;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2528 tgaaagtaaaaaaaaaaaaaaaaaaa 2554
||||||||||||||||||||||||||
Db 1334 tgaaagtaaaaaaaaaaaaaaaaaaa 1360

RESULT 14
AAF63820
ID AAF63820 standard; cDNA; 1721 BP.
XX
AC AAF63820;
XX
DT 03-APR-2001 (first entry)
XX
DE Human secreted protein gene 32 SEQ ID NO:42.
XX
KW Human; immunosuppressive; antiarthritic; antirheumatic; nootropic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
KW vulnerary; autoimmune disease; hyperproliferative disorder; cancer;
KW cardiovascular disorder; cerebrovascular disorder; infection;
KW nervous system disorder; ocular disorder; chemotaxis; food additive;
KW secreted protein; ss.
XX
OS Homo sapiens.
XX
PN WO200077021-A1.
XX
PD 21-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US15135.
XX
PR 11-JUN-1999; 99US-0138632.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM, Komatsoulis GA;
XX
DR WPI; 2001-071257/08.
DR P-PSDB; AAB75271.

XX
PT Nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT Parkinson's diseases and cancers -
XX
PS Claim 1; Page 457; 530pp; English.
XX
CC This invention relates to polynucleotide sequences AAF63789 - AAF63836
CC which encode human secreted proteins AAB75260 - AAB75287. Included in the
CC invention are protein sequences AAB75288 - AAB75341 which are fragments
CC of the secreted proteins and amino acid sequences with which these
CC fragments share homology. Examples of the activities of the proteins and
CC polynucleotides and the activities of their agonists and antagonists
CC include, immunosuppressive; antiarthritic; antirheumatic;
CC antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
CC nootropic; neuroprotective; antibacterial; virucide; fungicide;
CC opthalmalogical; and vulnerary activity. The protein and polynucleotide
CC sequences, their agonists and antagonists may be useful for treating,
CC preventing and diagnosing diseases and disorders such as autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders
CC e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities. Included in the invention are
CC oligonucleotides AAF63780 - AAF63788 and peptide AAB75239 which are used
CC in the identification and characterisation of the DNA and protein
CC sequences of the invention.
XX
SQ Sequence 1721 BP; 558 A; 294 C; 350 G; 519 T; 0 other;

Query Match 1.0%; Score 27; DB 22; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2528 tgaaagtaaaaaaaaaaaaaaaaaaa 2554
||||||||||||||||||||||||||
Db 1669 tgaaagtaaaaaaaaaaaaaaaaaaa 1695

RESULT 15
AAC67268
ID AAC67268 standard; cDNA; 3426 BP.
XX
AC AAC67268;
XX
DT 09-APR-2001 (first entry)
XX
DE Human NFAR-1 coding sequence SEQ ID NO: 1.
XX
KW Human; nuclear factor associated with dsRNA; NFAR-1; NFAR-2;
KW transcription regulator; chromosome 19p13.1-13.2; apoptosis;
KW tumourigenesis; ss.
XX
OS Homo sapiens.
XX
PN WO200077205-A1.
XX
PD 21-DEC-2000.
XX
PF 09-JUN-2000; 2000WO-US15767.
XX
PR 11-JUN-1999; 99US-0138612.
XX
PA (BARB/) BARBER G N.
PA (SAUN/) SAUNDERS L.
PA (PERK/) PERKINS D J.
XX
PI Barber GN, Saunders L, Perkins DJ;
XX
DR WPI; 2001-080688/09.
DR P-PSDB; AAB35147.
XX
PT Novel isolated human nuclear factor associated with dsRNA polypeptide
PT useful for determining structure-function relationships and as affinity
PT tag to identify and isolate interacting proteins that bind to the
PT factor -
XX
PS Claim 10; Page 45-47; 73pp; English.
XX
CC The present invention provides the protein and coding sequences of two
CC human nuclear factors associated with dsRNA (NFAR-1 and NFAR-2). These
CC are transcriptional regulators and are thought to play a role in
CC apoptosis and tumourigenesis. The coding sequence (found on chromosome
CC 19p13.1-13.2) is useful as a probe to detect rearrangements in tumour
CC cells and the protein is useful for determining structure-function
CC relationships.
XX
SQ Sequence 3426 BP; 886 A; 814 C; 913 G; 813 T; 0 other;

Query Match 1.0%; Score 27; DB 22; Length 3426;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2528 tgaaagtaaaaaaaaaaaaaaaaaaa 2554
||||||||||||||||||||||||||
Db 3398 tgaaagtaaaaaaaaaaaaaaaaaaa 3424

Search completed: August 27, 2001, 15:28:42
Job time: 6115 sec